



## **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/618,839  
Source: O/P/E  
Date Processed by STIC: 7/25/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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Revised 04/24/2003



OIEP

**RAW SEQUENCE LISTING**

PATENT APPLICATION: US/10/618,839

DATE: 07/25/2003

TIME: 07:58:42

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\07252003\J618839.raw

3 <110> APPLICANT: Lambeth, J. David  
 4 Cheng, Guangjie  
 5 McCoy, James  
 7 <120> TITLE OF INVENTION: Methods and Transgenic Mouse Model for Identifying and  
 Modulating Factors  
 8 Involved in the Production of Reactive Oxygen Intermediates  
 10 <130> FILE REFERENCE: 05501-0211 (43150-286808)  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/618,839  
 C--> 12 <141> CURRENT FILING DATE: 2003-07-14  
 12 <150> PRIOR APPLICATION NUMBER: US 60/395,498  
 13 <151> PRIOR FILING DATE: 2002-07-12  
 15 <160> NUMBER OF SEQ ID NOS: 19  
 17 <170> SOFTWARE: PatentIn version 3.1  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 2609  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Homo sapiens  
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 33 <223> OTHER INFORMATION: "n" = any nucleotide  
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 42 <220> FEATURE:  
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 44 <222> LOCATION: (2164)..(2164) ✓  
 45 <223> OTHER INFORMATION: "n" = any nucleotide  
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 50 <222> LOCATION: (2264)..(2264)  
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 57 ctcttggggt aggtgtgtgt ttttcacatc ttaaaggctc acagaccctg cgctggacaa 120  
 59 atgttccatt cctgaaggac ctctccagaa tccggattgc tgaatcttcc ctgttgcccta 180  
 61 gaagggtccc aaaccacctc ttgaca atg gga aac tgg gtg gtt aac cac tgg 233  
 62 Met Gly Asn Trp Val Val Asn His Trp  
 63 1 5

Does Not Comply  
 Corrected Diskette Needed

P.4

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\07252003\J618839.raw

65	ttt tca gtt ttg ttt ctg gtt gtt tgg tta ggg ctg aat gtt ttc ctg	281
66	Phe Ser Val Leu Phe Leu Val Val Trp Leu Gly Leu Asn Val Phe Leu	
67	10 15 20 25	
69	ttt gtg gat gcc ttc ctg aaa tat gag aag gcc gac aaa tac tac tac	329
70	Phe Val Asp Ala Phe Leu Lys Tyr Glu Lys Ala Asp Lys Tyr Tyr Tyr	
71	30 35 40	
73	aca aga aaa atc ctt ggg tca aca ttg gcc tgt gcc cga gcg tct gct	377
74	Thr Arg Lys Ile Leu Gly Ser Thr Leu Ala Cys Ala Arg Ala Ser Ala	
75	45 50 55	
77	ctc tgc ttg aat ttt aac agc acg ctg atc ctg ctt cct gtg tgt cgc	425
78	Leu Cys Leu Asn Phe Asn Ser Thr Leu Ile Leu Leu Pro Val Cys Arg	
79	60 65 70	
81	aat ctg ctg tcc ttc ctg agg ggc acc tgc tca ttt tgc agc cgc aca	473
82	Asn Leu Leu Ser Phe Leu Arg Gly Thr Cys Ser Phe Cys Ser Arg Thr	
83	75 80 85	
85	ctg aga aag caa ttg gat cac aac ctc acc ttc cac aag ctg gtg gcc	521
86	Leu Arg Lys Gln Leu Asp His Asn Leu Thr Phe His Lys Leu Val Ala	
87	90 95 100 105	
89	tat atg atc tgc cta cat aca gct att cac atc att gca cac ctg ttt	569
90	Tyr Met Ile Cys Leu His Thr Ala Ile His Ile Ile Ala His Leu Phe	
91	110 115 120	
93	aac ttt gac tgc tat agc aga agc cga cag gcc aca gat ggc tcc ctt	617
94	Asn Phe Asp Cys Tyr Ser Arg Ser Arg Gln Ala Thr Asp Gly Ser Leu	
95	125 130 135	
97	gcc tcc att ctc tcc agc cta tct cat gat gag aaa aag ggg ggt tct	665
98	Ala Ser Ile Leu Ser Ser Leu Ser His Asp Glu Lys Lys Gly Gly Ser	
99	140 145 150	
101	tgg cta aat ccc atc cag tcc cga aac acg aca gtg gag tat gtg aca	713
102	Trp Leu Asn Pro Ile Gln Ser Arg Asn Thr Thr Val Glu Tyr Val Thr	
103	155 160 165	
105	ttc acc agc gtt gct ggt ctc act gga gtg atc atg aca ata gcc ttg	761
106	Phe Thr Ser Val Ala Gly Leu Thr Gly Val Ile Met Thr Ile Ala Leu	
107	170 175 180 185	
109	att ctc atg gta act tca gct act gag ttc atc cgg agg agt tat ttt	809
110	Ile Leu Met Val Thr Ser Ala Thr Glu Phe Ile Arg Arg Ser Tyr Phe	
111	190 195 200	
113	gaa gtc ttc tgg tat act cac cac ctt ttt atc ttc tat atc ctt ggc	857
114	Glu Val Phe Trp Tyr Thr His His Leu Phe Ile Phe Tyr Ile Leu Gly	
115	205 210 215	
117	tta ggg att cac ggc att ggt gga att gtc cgg ggt caa aca gag gag	905
118	Leu Gly Ile His Gly Ile Gly Gly Ile Val Arg Gly Gln Thr Glu Glu	
119	220 225 230	
121	agc atg aat gag agt cat cct cgc aag tgt gca gag tct ttt gag atg	953
122	Ser Met Asn Glu Ser His Pro Arg Lys Cys Ala Glu Ser Phe Glu Met	
123	235 240 245	
125	tgg gat gat cgt gac tcc cac tgt agg cgc cct aag ttt gaa ggg cat	1001
126	Trp Asp Asp Arg Asp Ser His Cys Arg Arg Pro Lys Phe Glu Gly His	
127	250 255 260 265	
129	ccc cct gag tct tgg aag tgg atc ctt gca ccg gtc att ctt tat atc	1049

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130	Pro	Pro	Glu	Ser	Trp	Lys	Trp	Ile	Leu	Ala	Pro	Val	Ile	Leu	Tyr	Ile	
131					270					275					280		
133	tgt	gaa	agg	atc	ctc	cgg	ttt	tac	cgc	tcc	cag	cag	aag	gtt	gtg	att	1097
134	Cys	Glu	Arg	Ile	Leu	Arg	Phe	Tyr	Arg	Ser	Gln	Gln	Lys	Val	Val	Ile	
135				285					290					295			
137	acc	aag	gtt	gtt	atg	cac	cca	tcc	aaa	gtt	ttg	gaa	ttg	cag	atg	aac	1145
138	Thr	Lys	Val	Val	Met	His	Pro	Ser	Lys	Val	Leu	Glu	Leu	Gln	Met	Asn	
139			300					305					310				
141	aag	cgt	ggc	ttc	agc	atg	gaa	gtg	ggg	cag	tat	atc	ttt	gtt	aat	tgc	1193
142	Lys	Arg	Gly	Phe	Ser	Met	Glu	Val	Gly	Gln	Tyr	Ile	Phe	Val	Asn	Cys	
143		315					320					325					
145	ccc	tca	atc	tct	ctc	ctg	gaa	tgg	cat	cct	ttt	act	ttg	acc	tct	gct	1241
146	Pro	Ser	Ile	Ser	Leu	Leu	Glu	Trp	His	Pro	Phe	Thr	Leu	Thr	Ser	Ala	
147	330					335				340						345	
149	cca	gag	gaa	gat	ttc	ttc	tcc	att	cat	atc	cga	gca	gca	ggg	gac	tgg	1289
150	Pro	Glu	Glu	Asp	Phe	Phe	Ser	Ile	His	Ile	Arg	Ala	Ala	Gly	Asp	Trp	
151				350					355					360			
153	aca	gaa	aat	ctc	ata	agg	gct	ttc	gaa	caa	caa	tat	tca	cca	att	ccc	1337
154	Thr	Glu	Asn	Leu	Ile	Arg	Ala	Phe	Glu	Gln	Gln	Tyr	Ser	Pro	Ile	Pro	
155			365					370					375				
157	agg	att	gaa	gtg	gat	ggg	ccc	ttt	ggc	aca	gcc	agt	gag	gat	gtt	ttc	1385
158	Arg	Ile	Glu	Val	Asp	Gly	Pro	Phe	Gly	Thr	Ala	Ser	Glu	Asp	Val	Phe	
159			380				385					390					
161	cag	tat	gaa	gtg	gct	gtg	ctg	gtt	gga	gca	gga	att	ggg	gtc	acc	ccc	1433
162	Gln	Tyr	Glu	Val	Ala	Val	Leu	Val	Gly	Ala	Gly	Ile	Gly	Val	Thr	Pro	
163		395				400					405						
165	ttt	gct	tct	atc	ttg	aaa	tcc	atc	tgg	tac	aaa	ttc	cag	tgt	gca	gac	1481
166	Phe	Ala	Ser	Ile	Leu	Lys	Ser	Ile	Trp	Tyr	Lys	Phe	Gln	Cys	Ala	Asp	
167	410				415				420							425	
169	cac	aac	ctc	aaa	aca	aaa	aag	atc	tat	ttc	tac	tgg	atc	tgc	agg	gag	1529
170	His	Asn	Leu	Lys	Thr	Lys	Lys	Ile	Tyr	Phe	Tyr	Trp	Ile	Cys	Arg	Glu	
171				430					435					440			
173	aca	ggg	gcc	ttt	tcc	tgg	ttc	aac	aac	ctg	ttg	act	tcc	ctg	gaa	cag	1577
174	Thr	Gly	Ala	Phe	Ser	Trp	Phe	Asn	Asn	Leu	Leu	Thr	Ser	Leu	Glu	Gln	
175			445					450					455				
177	gag	atg	gag	gaa	tta	ggc	aaa	gtg	ggg	ttt	cta	aac	tac	cgt	ctc	ttc	1625
178	Glu	Met	Glu	Glu	Leu	Gly	Lys	Val	Gly	Phe	Leu	Asn	Tyr	Arg	Leu	Phe	
179			460				465					470					
181	ctc	acc	gga	tgg	gac	agc	aat	att	gtt	ggg	cat	gca	gca	tta	aac	ttt	1673
182	Leu	Thr	Gly	Trp	Asp	Ser	Asn	Ile	Val	Gly	His	Ala	Ala	Leu	Asn	Phe	
183		475				480					485						
185	gac	aag	gcc	act	gac	atc	gtg	aca	ggg	ctg	aaa	cag	aaa	acc	tcc	ttt	1721
186	Asp	Lys	Ala	Thr	Asp	Ile	Val	Thr	Gly	Leu	Lys	Gln	Lys	Thr	Ser	Phe	
187	490				495				500							505	
189	ggg	aga	cca	atg	tgg	gac	aat	gag	ttt	tct	aca	ata	gct	acc	tcc	cac	1769
190	Gly	Arg	Pro	Met	Trp	Asp	Asn	Glu	Phe	Ser	Thr	Ile	Ala	Thr	Ser	His	
191				510				515					520				
193	ccc	aag	tct	gta	gtg	gga	gtt	ttc	tta	tgt	ggc	cct	cgg	act	ttg	gca	1817
194	Pro	Lys	Ser	Val	Val	Gly	Val	Phe	Leu	Cys	Gly	Pro	Arg	Thr	Leu	Ala	

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195 525 530 535  
 197 aag agc ctg cgc aaa tgc tgt cac cga tat tcc agt ctg gat cct aga 1865  
 198 Lys Ser Leu Arg Lys Cys Cys His Arg Tyr Ser Ser Leu Asp Pro Arg  
 199 540 545 550  
 201 aag gtt caa ttc tac ttc aac aaa gaa aat ttt tga gttataggaa 1911  
 202 Lys Val Gln Phe Tyr Phe Asn Lys Glu Asn Phe  
 203 555 560  
 205 taaggacggt aatctgcatt ttgtctcttt gtatcttcag taattgagtt atagggaataa 1971  
**W--> 207 ggacggtaaat ctgcattttt tctcttttga tcttcagtaa tttacttggt ctcttcaggt 2031**  
 209 ttgancagtc actttaggat aagaatgtgc ctctcaagcc ttgactccct ggtattcttt 2091  
 211 ttttgattgc attcaacttc gttacttgag cttcagcaac ttaagaactt ctgaagttct 2151  
 213 taaagtcttg aantttctta agcccatgga tcttttctca gaaaaataac tgtaaattctt 2211  
 215 tctggacagc catgactgta gcaaggcttg atagcagaag tttggtggtt canaattata 2271  
 217 caactaatcc caggtgattt tatcaattcc agtgttacca tctcctgagt tttggtttgt 2331  
 219 aatcttttgt cctctccacc cccacagaag attttaagta gggtagcttt ttaaataaaa 2391  
 221 atttattgaa taattaatga taaaacataa taataaacat aaataataaa caaaattacc 2451  
 223 gagaacccca tccccatata acaccaacag tgtacatgtt tactgtcact tttgatattg 2511  
 225 tttatccagt gtgaacagca atttattatt tttgtctatc aaaaaataaa ggattttttt 2571  
 227 tcacttgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 2609  
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 232 <212> TYPE: PRT  
 233 <213> ORGANISM: Homo sapiens  
 235 <220> FEATURE:  
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 238 <223> OTHER INFORMATION: "n" = any nucleotide  
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 262 20 25 30  
 265 Tyr Glu Lys Ala Asp Lys Tyr Tyr Tyr Thr Arg Lys Ile Leu Gly Ser  
 266 35 40 45  
 269 Thr Leu Ala Cys Ala Arg Ala Ser Ala Leu Cys Leu Asn Phe Asn Ser  
 270 50 55 60  
 273 Thr Leu Ile Leu Leu Pro Val Cys Arg Asn Leu Leu Ser Phe Leu Arg

*These do not apply to  
 this sequence. Only  
 564 residues in this  
 sequence; it is also  
 a peptide sequence*

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274	65					70				75				80		
277	Gly	Thr	Cys	Ser	Phe	Cys	Ser	Arg	Thr	Leu	Arg	Lys	Gln	Leu	Asp	His
278					85					90				95		
281	Asn	Leu	Thr	Phe	His	Lys	Leu	Val	Ala	Tyr	Met	Ile	Cys	Leu	His	Thr
282				100					105					110		
285	Ala	Ile	His	Ile	Ile	Ala	His	Leu	Phe	Asn	Phe	Asp	Cys	Tyr	Ser	Arg
286			115					120					125			
289	Ser	Arg	Gln	Ala	Thr	Asp	Gly	Ser	Leu	Ala	Ser	Ile	Leu	Ser	Ser	Leu
290		130					135					140				
293	Ser	His	Asp	Glu	Lys	Lys	Gly	Gly	Ser	Trp	Leu	Asn	Pro	Ile	Gln	Ser
294	145					150					155					160
297	Arg	Asn	Thr	Thr	Val	Glu	Tyr	Val	Thr	Phe	Thr	Ser	Val	Ala	Gly	Leu
298					165					170					175	
301	Thr	Gly	Val	Ile	Met	Thr	Ile	Ala	Leu	Ile	Leu	Met	Val	Thr	Ser	Ala
302				180					185					190		
305	Thr	Glu	Phe	Ile	Arg	Arg	Ser	Tyr	Phe	Glu	Val	Phe	Trp	Tyr	Thr	His
306			195					200					205			
309	His	Leu	Phe	Ile	Phe	Tyr	Ile	Leu	Gly	Leu	Gly	Ile	His	Gly	Ile	Gly
310		210					215						220			
313	Gly	Ile	Val	Arg	Gly	Gln	Thr	Glu	Glu	Ser	Met	Asn	Glu	Ser	His	Pro
314	225					230					235					240
317	Arg	Lys	Cys	Ala	Glu	Ser	Phe	Glu	Met	Trp	Asp	Asp	Arg	Asp	Ser	His
318					245					250					255	
321	Cys	Arg	Arg	Pro	Lys	Phe	Glu	Gly	His	Pro	Pro	Glu	Ser	Trp	Lys	Trp
322				260					265					270		
325	Ile	Leu	Ala	Pro	Val	Ile	Leu	Tyr	Ile	Cys	Glu	Arg	Ile	Leu	Arg	Phe
326			275					280					285			
329	Tyr	Arg	Ser	Gln	Gln	Lys	Val	Val	Ile	Thr	Lys	Val	Val	Met	His	Pro
330		290					295					300				
333	Ser	Lys	Val	Leu	Glu	Leu	Gln	Met	Asn	Lys	Arg	Gly	Phe	Ser	Met	Glu
334	305					310					315					320
337	Val	Gly	Gln	Tyr	Ile	Phe	Val	Asn	Cys	Pro	Ser	Ile	Ser	Leu	Leu	Glu
338					325					330					335	
341	Trp	His	Pro	Phe	Thr	Leu	Thr	Ser	Ala	Pro	Glu	Glu	Asp	Phe	Phe	Ser
342				340					345					350		
345	Ile	His	Ile	Arg	Ala	Ala	Gly	Asp	Trp	Thr	Glu	Asn	Leu	Ile	Arg	Ala
346			355					360					365			
349	Phe	Glu	Gln	Gln	Tyr	Ser	Pro	Ile	Pro	Arg	Ile	Glu	Val	Asp	Gly	Pro
350		370					375					380				
353	Phe	Gly	Thr	Ala	Ser	Glu	Asp	Val	Phe	Gln	Tyr	Glu	Val	Ala	Val	Leu
354	385					390					395					400
357	Val	Gly	Ala	Gly	Ile	Gly	Val	Thr	Pro	Phe	Ala	Ser	Ile	Leu	Lys	Ser
358					405					410					415	
361	Ile	Trp	Tyr	Lys	Phe	Gln	Cys	Ala	Asp	His	Asn	Leu	Lys	Thr	Lys	Lys
362				420					425					430		
365	Ile	Tyr	Phe	Tyr	Trp	Ile	Cys	Arg	Glu	Thr	Gly	Ala	Phe	Ser	Trp	Phe
366			435					440					445			
369	Asn	Asn	Leu	Leu	Thr	Ser	Leu	Glu	Gln	Glu	Met	Glu	Glu	Leu	Gly	Lys
370		450					455					460				

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/618,839

DATE: 07/25/2003  
TIME: 07:58:43

Input Set : A:\PTO.YF.txt  
Output Set: N:\CRF4\07252003\J618839.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 2025,2036,2164,2264

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7

**VERIFICATION SUMMARY**PATENT APPLICATION: **US/10/618,839**

DATE: 07/25/2003

TIME: 07:58:43

Input Set : **A:\PTO.YF.txt**Output Set: **N:\CRF4\07252003\J618839.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:36 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27  
L:207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1971  
M:341 Repeated in SeqNo=1  
L:412 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:409  
L:734 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:731  
L:1056 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:1053  
L:1388 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:1385  
L:1714 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:1711  
L:2570 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:2567